RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/713,578_

Source: _TFwo_

Date Processed by STIC: _1/3/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 4.2 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04): U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/713,578_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

·2____Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.

4____Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as **required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.**

5____Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum number of each** residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
(OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8____Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10____Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11____Use of <220>
Sequence(s)_____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

FYI

12_____PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____ Misuse of n/Xaa
"n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

RAW SEQUENCE LISTING   DATE: 01/03/2005
PATENT APPLICATION: US/10/713,578   TIME: 15:44:38

Input Set : A:\124263-1006 SEQUENCE LISTING.ST25.txt
Output Set: N:\CRF4\01032005\J713578.raw

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 3 <110> APPLICANT: Awasthi, Sanjay
 4         Singhal, Sharad S.
 6 <120> TITLE OF INVENTION: Liposomes For Protection Against Toxic Compounds
 8 <130> FILE REFERENCE: 124263-1006
10 <140> CURRENT APPLICATION NUMBER: US 10/713,578
11 <141> CURRENT FILING DATE: 2003-11-13
13 <150> PRIOR APPLICATION NUMBER: 60/425,814
14 <151> PRIOR FILING DATE: 2002-11-13
16 <160> NUMBER OF SEQ ID NOS: 2
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 655
22 <212> TYPE: PRT
23 <213> ORGANISM: recombinant
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35 Ile Ser Pro Thr Lys Phe Pro Gly Leu Tyr Arg Thr Gly Glu Pro Ser
36          35                  40                  45
39 Pro Pro His Asp Ile Leu His Glu Pro Pro Asp Tyr Val Ser Asp Asp
40      50                  55                  60
43 Glu Lys Asp His Gly Lys Lys Lys Gly Lys Phe Lys Lys Lys Glu Lys
44 65                  70                  75                  80
47 Arg Thr Glu Gly Tyr Ala Ala Phe Gln Glu Asp Ser Ser Gly Asp Glu
48              85                  90                  95
51 Ala Glu Ser Pro Ser Lys Met Lys Arg Ser Lys Gly Ile His Val Phe
52              100                 105                 110
55 Lys Lys Pro Ser Phe Ser Lys Lys Lys Glu Lys Asp Phe Lys Ile Lys
56          115                 120                 125
59 Glu Lys Pro Lys Glu Glu Lys His Lys Glu Glu Lys His Lys Glu Glu
60      130                 135                 140
63 Lys His Lys Glu Lys Lys Ser Lys Asp Leu Thr Ala Ala Asp Val Val
64 145                 150                 155                 160
67 Lys Gln Trp Lys Glu Lys Lys Lys Lys Lys Pro Ile Gln Glu Pro
68              165                 170                 175
71 Glu Val Pro Gln Ile Asp Val Pro Asn Leu Lys Pro Ile Phe Gly Ile
72          180                 185                 190
75 Pro Leu Ala Asp Ala Val Glu Arg Thr Met Met Tyr Asp Gly Ile Arg
76          195                 200                 205
79 Leu Pro Ala Val Phe Arg Glu Cys Ile Asp Tyr Val Glu Lys Tyr Gly
80      210                 215                 220
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83  Met Lys Cys Glu Gly Ile Tyr Arg Val Ser Gly Ile Lys Ser Lys Val
84  225                 230                 235                 240
87  Asp Glu Leu Lys Ala Ala Tyr Asp Arg Glu Glu Ser Thr Asn Leu Lys
88                  245                 250                 255
91  Asp Tyr Glu Pro Asn Thr Val Ala Ser Leu Leu Lys Gln Tyr Leu Arg
92              260                 265                 270
95  Asp Leu Pro Glu Asn Leu Leu Thr Lys Glu Leu Met Pro Arg Phe Glu
96          275                 280                 285
99  Glu Ala Cys Gly Arg Thr Thr Glu Thr Glu Lys Val Gln Glu Phe Gln
100     290                 295                 300
103 Arg Leu Leu Lys Arg Leu Pro Glu Cys Asn Tyr Leu Leu Ile Ser Trp
104 305                 310                 315                 320
107 Leu Ile Val His Met Asp His Val Ile Ala Lys Glu Leu Glu Thr Lys
108                 325                 330                 335
111 Met Asn Ile Gln Asn Ile Ser Ile Val Leu Ser Pro Thr Val Gln Ile
112             340                 345                 350
115 Ser Asn Arg Val Leu Tyr Val Phe Phe Thr His Val Gln Glu Leu Phe
116         355                 360                 365
119 Gly Asn Val Val Leu Lys Gln Val Met Lys Pro Leu Arg Trp Ser Asn
120     370                 375                 380
123 Met Ala Thr Met Pro Thr Leu Pro Glu Thr Gln Ala Gly Ile Lys Glu
124 385                 390                 395                 400
127 Glu Ile Arg Arg Gln Glu Phe Leu Leu Asn Cys Leu His Arg Asp Leu
128                 405                 410                 415
131 Gln Gly Gly Ile Lys Asp Leu Ser Lys Glu Lys Arg Leu Trp Glu Val
132             420                 425                 430
135 Gln Arg Ile Leu Thr Ala Leu Lys Arg Lys Leu Arg Glu Ala Lys Arg
136         435                 440                 445
139 Gln Glu Cys Glu Thr Lys Ile Ala Gln Glu Ile Ala Ser Leu Ser Lys
140     450                 455                 460
143 Glu Asp Val Ser Lys Glu Glu Met Asn Glu Asn Lys Glu Val Ile Asn
144 465                 470                 475                 480
147 Ile Leu Leu Ala Gln Glu Asn Glu Ile Leu Thr Glu Gln Glu Glu Leu
148                 485                 490                 495
151 Leu Ala Asn Glu Gln Phe Leu Arg Arg Gln Ile Ala Ser Glu Lys Glu
152             500                 505                 510
155 Glu Ile Glu Arg Leu Arg Ala Glu Ile Ala Glu Ile Gln Ser Arg Gln
156         515                 520                 525
159 Gln His Gly Arg Ser Glu Thr Glu Glu Tyr Ser Ser Glu Ser Glu Ser
160     530                 535                 540
163 Glu Ser Glu Asp Glu Glu Glu Leu Gln Ile Ile Leu Glu Asp Leu Gln
164 545                 550                 555                 560
167 Arg Gln Asn Glu Glu Leu Glu Ile Lys Asn Asn His Leu Asn Gln Ala
168             565                 570                 575
171 Ile His Glu Glu Arg Glu Ala Ile Ile Glu Leu Arg Val Gln Leu Arg
172         580                 585                 590
175 Leu Leu Gln Met Gln Arg Ala Lys Ala Glu Gln Gln Ala Gln Glu Asp
176         595                 600                 605
179 Glu Glu Pro Glu Trp Arg Gly Gly Ala Val Gln Pro Pro Arg Asp Gly
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180      610                615                620
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193 <212> TYPE: DNA
194 <213> ORGANISM: human bone marrow
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201 ttgtaccgca ctggcgagcc ctcacctccc catgacatcc tcatgagcct cctgatgtag   180
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207 ctaaaatgaa gaggtccaag ggaatccatg ttttcaagaa gaagcccagc ttttctaaaa   360
209 agaaggaaaa ggattttaaa ataaaagaga aacccaaaga agaaagcat aaagaagaaa   420
211 gcacaaagaa gaaaaacata aagagaagaa gtcaaaagac ttgacagcag ctgatgttgt   480
213 taaacagtgg aaggaaaaga agaaaaagaa aaagccaatt caggagccag aggtgcctca   540
215 gattgatgtt ccaaatctca aacccatttt tggaattcct ttggctgatg cagtagagag   600
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VERIFICATION SUMMARY   DATE: 01/03/2005
PATENT APPLICATION: **US/10/713,578**   TIME: 15:44:39

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